

SEQUENCE LISTING

<110> Wang, Baiyang

<120> Tissue Factor Antibodies and Uses Thereof

<130> 1861.1670002

<160> 35

<170> PatentIn version 3.2

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<220>

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<222> (1) .. (915)

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Ala Arg Thr Leu Leu Leu Gly Trp Val Phe Ala Gln Val Ala Gly Ala	
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tca ggc act aca aat act gtg gca gca tat aat tta act tgg aaa tca	144
Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser	
35 40 45	
act aat ttc aag aca att ttg gag tgg gaa ccc aaa ccc gtc aat caa	192
Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln	
50 55 60	
gtc tac act gtt caa ata agc act aag tca gga gat tgg aaa agc aaa	240
Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys	
65 70 75 80	
tgc ttt tac aca aca gac aca gag tgt gac ctc acc gac gag att gtg	288
Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val	
85 90 95	
aag gat gtg aag cag acg tac ttg gca cgg gtc ttc tcc tac ccg gca	336
Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala	
100 105 110	
ggg aat gtg gag agc acc ggt tct gct ggg gag cct ctg tat gag aac	384
Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn	
115 120 125	
tcc cca gag ttc aca cct tac ctg gag aca aac ctc gga cag cca aca	432
Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr	
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Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu	

145	150	155	160	
gat gaa cgg act tta gtc aga agg aac aac act ttc cta agc ctc cgg				528
Asp Glu Arg Thr	Leu Val Arg Arg	Asn Asn Thr Phe	Leu Ser Leu Arg	
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Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu				
	195	200	205	
att gat gtg gat aaa gga gaa aac tac tgt ttc agt gtt caa gca gtg				672
Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val				
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	225	230	235	240
tgt atg ggc cag gag aaa ggg gaa ttc aga gaa ata ttc tac atc att				768
Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Ile Phe Tyr Ile Ile				
	245	250	255	
gga gct gtg gta ttt gtg gtc atc atc ctt gtc atc atc ctg gct ata				816
Gly Ala Val Val Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile				
	260	265	270	
tct cta cac aag tgt aga aag gca gga gtg ggg cag agc tgg aag gag				864
Ser Leu His Lys Cys Arg Lys Ala Gly Val Gly Gln Ser Trp Lys Glu				
	275	280	285	
aac tcc cca ctg aat gtt tca aga gga tcc cac cat cac cat cac cat				912
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Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser			
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Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln			

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Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys				
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Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val				
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Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala				
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Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn				
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Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr				
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Ile Gln Ser Phe Glu Gln Val Gly Thr Lys Val Asn Val Thr Val Glu				
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Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg				
	165	170		175
Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser				
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Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu				
	195	200		205
Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val				
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Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu				
225	230	235		240
Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Ile Phe Tyr Ile Ile				
	245	250		255
Gly Ala Val Val Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile				
	260	265		270
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 tca ggc act aca aat act gtg gca gca tat aat tta act tgg aaa tca 144  
 Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser  
 35 40 45  
 act aat ttc aag aca att ttg gag tgg gaa ccc aaa ccc gtc aat caa 192  
 Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln  
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 gtc tac act gtt caa ata agc act aag tca gga gat tgg aaa agc aaa 240  
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 65 70 75 80  
 tgc ttt tac aca aca gac aca gag tgt gac ctc acc gac gag att gtg 288  
 Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val  
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 Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala  
 100 105 110  
 ggg aat gtg gag agc acc ggt tct gct ggg gag cct ctg tat gag aac 384  
 Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn  
 115 120 125  
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 Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr  
 130 135 140  
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 Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser  
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Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu	
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Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val	
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Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu	
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tgt atg ggc cag gag aaa ggg gaa ttc aga gaa aga gga tcc cac cat	768
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35 40 45

Thr Asn Phe Lys Thr Ile Leu Glu Trp Glu Pro Lys Pro Val Asn Gln
50 55 60

Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly Asp Trp Lys Ser Lys
65 70 75 80

Cys Phe Tyr Thr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val
85 90 95

Lys Asp Val Lys Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala
100 105 110

Gly Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu Tyr Glu Asn
115 120 125

Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr
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Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu Arg		
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Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Tyr Trp Lys Ser		
	180	185 190
Ser Ser Ser Gly Lys Lys Thr Ala Lys Thr Asn Thr Asn Glu Phe Leu		
	195	200 205
Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val		
	210	215 220
Ile Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu		
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Cys Met Gly Gln Glu Lys Gly Glu Phe Arg Glu Arg Gly Ser His His		
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Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr	
20 25 30	
tgg ata gag tgg gta aag cag agg cct gga cat ggc ctt gag tgg att	144
Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile	
35 40 45	
gga gag att tta cct gga agt ggt agt act aac tac aat gag aag ttc	192
Gly Glu Ile Leu Pro Gly Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe	
50 55 60	

aag ggc aag gcc aca ttc act gca gat aca tcc tcc aac aca gcc tac 240  
Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr  
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atg caa ctc agc agc ctg aca tct gag gac tct gcc gtc tat tac tgt 288  
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85 90 95

gca aga gag gat agg tac gac ggt gac tac tgg ggc caa ggc acc act 336  
Ala Arg Glu Asp Arg Tyr Asp Gly Asp Tyr Trp Gly Gln Gly Thr Thr  
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Leu Thr Val Ser  
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35 40 45

Gly Glu Ile Leu Pro Gly Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe  
50 55 60

Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr  
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Glu Asp Arg Tyr Asp Gly Asp Tyr Trp Gly Gln Gly Thr Thr  
100 105 110

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aca gtc aca ctc act tgt cgc tca agt act ggg gct gtt aca act agt	96
Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser	
20 25 30	
aac tat gcc aac tgg gtc caa gaa aaa cca gat cat tta ttc act ggt	144
Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly	
35 40 45	
cta ata ggt ggt acc aac aac cga gct cca ggt gtt cct gcc aga ttc	192
Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe	
50 55 60	
tca ggc tcc ctg att gga gac aag gct gcc ctc acc atc aca ggg gca	240
Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala	
65 70 75 80	
cag act gag gat gag gca ata tat ttc tgt gct cta tgg tac agc aac	288
Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn	
85 90 95	
cac tgg gtg ttc ggt gga gga acc aaa ctg act gtc cta ggt cag ccc c	337
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35 40 45	
Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe	
50 55 60	
Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala	
65 70 75 80	



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85 90 95

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tca gtg aag ata tcc tgc aag gct tct ggt tac tca ttc act ggc tac 96  
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr  
20 25 30  
aac atg aac tgg gtg aag cag agc aat gga aag agc ctt gag tgg att 144  
Asn Met Asn Trp Val Lys Gln Ser Asn Gly Lys Ser Leu Glu Trp Ile  
35 40 45  
gga aat att gat cct tac tat ggt ggt act agc tac aac cag aag ttc 192  
Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe  
50 55 60  
aag ggc aag gcc aca ttg act gta gac aaa tcc tcc aac aca gcc tac 240  
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr  
65 70 75 80  
atg cac ctc aag agc ctg aca tct gag gac tct gca gtc tat tac tgt 288  
Met His Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95  
gca aga gat agt agc tcc tgg ttt gct tac tgg ggc caa ggg act ctg 336  
Ala Arg Asp Ser Ser Ser Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu  
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Val Thr Val Ser Ala  
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35 40 45

Gly Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Ser Tyr Asn Gln Lys Phe  
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Asn Thr Ala Tyr  
65 70 75 80

Met His Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95

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100 105 110

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gaa act gtc acc atc aca tgt cga gca agt ggg aat att cac aat tat 96  
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Gly Asn Ile His Asn Tyr  
20 25 30  
tta gca tgg tat cag cag aaa cag gga aaa tct cct cag ctc ctg gtc 144  
Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val  
35 40 45  
tat aat gca aaa acc tta gca gat ggt gtg cca tca agg ttc agt ggc 192  
Tyr Asn Ala Lys Thr Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60  
agt gga tca gga aca caa tat tct ctc aag atc aac agc ctg cag cct 240  
Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Pro

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gaa gat ttt ggg agt tat tac tgt caa cat ttt tgg att act ccg tgg								288								
Glu	Asp	Phe	Gly	Ser	Tyr	Tyr	Cys	Gln	His	Phe	Trp	Ile	Thr	Pro	Trp	
				85					90					95		

acg ttc ggt gga ggc acc aag ctg gag atc taa cgg a																325
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			100						105							

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			20					25					30		

Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Gln	Gly	Lys	Ser	Pro	Gln	Leu	Leu	Val
		35					40					45			

Tyr	Asn	Ala	Lys	Thr	Leu	Ala	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
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Ser	Gly	Ser	Gly	Thr	Gln	Tyr	Ser	Leu	Lys	Ile	Asn	Ser	Leu	Gln	Pro
65					70					75				80	

Glu	Asp	Phe	Gly	Ser	Tyr	Tyr	Cys	Gln	His	Phe	Trp	Ile	Thr	Pro	Trp
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Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Thr	Gly	Tyr	Thr	Phe	Ser	Ser	Tyr		
			20				25					30					
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Trp	Ile	Glu	Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly	Leu	Glu	Trp	Ile		
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gga	gag	att	tta	cct	gga	agt	gct	agt	act	aag	tac	aat	gag	aag	ttc		192
Gly	Glu	Ile	Leu	Pro	Gly	Ser	Ala	Ser	Thr	Lys	Tyr	Asn	Glu	Lys	Phe		
	50				55					60							
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Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys		
			85					90					95				
gca	agag	gat	tat	tac	tac	ggt	agt	agc	tac	ggg	ttt	gct	tac	tgg	ggc		336
Ala	Arg	Asp	Tyr	Tyr	Tyr	Gly	Ser	Ser	Tyr	Gly	Phe	Ala	Tyr	Trp	Gly		
			100				105					110					
caa	ggg	act	ctg	gtc	act	gtc	tcg	agt									363
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser									
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Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Thr	Gly	Tyr	Thr	Phe	Ser	Ser	Tyr		
			20				25					30					
Trp	Ile	Glu	Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly	Leu	Glu	Trp	Ile		
		35				40					45						
Gly	Glu	Ile	Leu	Pro	Gly	Ser	Ala	Ser	Thr	Lys	Tyr	Asn	Glu	Lys	Phe		
	50				55					60							
Lys	Gly	Lys	Ala	Thr	Phe	Thr	Ala	Asp	Thr	Ser	Ser	Asn	Thr	Ala	Tyr		
65				70				75						80			
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys		
			85				90							95			

Ala Arg Asp Tyr Tyr Tyr Gly Ser Ser Tyr Gly Phe Ala Tyr Trp Gly  
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 20  
<211> 330  
<212> DNA  
<213> Mus sp.

<220>  
<221> CDS  
<222> (1)..(330)

<400> 20  
cag gct gtt gtg act cag gaa tct gca ctc acc aca tca cct ggt gaa 48  
Gln Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu  
1 5 10 15  
aca gtc aca ctc act tgt cgc tca agt act ggg gct gtt aca act agt 96  
Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser  
20 25 30  
aac tat gcc aac tgg gtc caa gaa aaa cca gat cat tta ttc act ggc 144  
Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly  
35 40 45  
cta ata ggt ggt acc aac aac cga ggt cca ggt gtt cct gcc aga ttc 192  
Leu Ile Gly Gly Thr Asn Asn Arg Gly Pro Gly Val Pro Ala Arg Phe  
50 55 60  
tca ggc tcc ctg att gga gac aag gct gcc ctc acc atc aca ggg gca 240  
Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala  
65 70 75 80  
cag act gag gat gag gca gta tat ttc tgt gct cta tgg tac agc aac 288  
Gln Thr Glu Asp Glu Ala Val Tyr Phe Cys Ala Leu Trp Tyr Ser Asn  
85 90 95  
cat tgg gtg ttc ggt gga gga acc aaa ctg act gtc cta ggt 330  
His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

<210> 21  
<211> 110  
<212> PRT  
<213> Mus sp.

<400> 21

Gln Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu  
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser  
20 25 30

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly  
35 40 45

Leu Ile Gly Gly Thr Asn Asn Arg Gly Pro Gly Val Pro Ala Arg Phe  
50 55 60

Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala  
65 70 75 80

Gln Thr Glu Asp Glu Ala Val Tyr Phe Cys Ala Leu Trp Tyr Ser Asn  
85 90 95

His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
100 105 110

<210> 22  
<211> 354  
<212> DNA  
<213> Mus sp.

<220>  
<221> CDS  
<222> (1) .. (354)

<400> 22  
cag gtc caa ctg cag cag cct ggg gct gag ctt gtg aag cct ggg gct 48  
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala  
1 5 10 15  
tca gtg aag ctg tcc tgc aag act tct ggc tac acc ttc acc agc tac 96  
Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Ser Tyr  
20 25 30  
tgg atg cac tgg gtg aag cag agg cct gga caa ggc ctt gag tgg atc 144  
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45  
gga gag att gat cct tct gat agt tat act aac tac aat caa aag ttc 192  
Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe  
50 55 60  
aag ggc aag gcc aca ttg act gta gac aaa tcc tcc agc aca gcc tac 240  
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80  
atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc tat tac tgt 288  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95  
acc tac tat gtt aac tac tat gct atg gac tac tgg ggt caa gga acc 336  
Thr Tyr Tyr Val Asn Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr

100 105 110 354  
tca gtc acc gtc tcc tca  
Ser Val Thr Val Ser Ser  
115

<210> 23  
<211> 118  
<212> PRT  
<213> Mus sp.

<400> 23

Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala  
1 5 10 15

Ser Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Ser Tyr  
20 25 30

Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe  
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95

Thr Tyr Tyr Val Asn Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr  
100 105 110

Ser Val Thr Val Ser Ser  
115

<210> 24  
<211> 318  
<212> DNA  
<213> Mus sp.

<220>  
<221> CDS  
<222> (1)..(318)

<400> 24 48  
caa att gtt ctc acc cag tct cca gca atc atg tct gca tct cta ggg  
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Leu Gly  
1 5 10 15



gag gag atc acc cta acc tgc agt gcc agc tcg agt gta agt tac atg 96  
 Glu Glu Ile Thr Leu Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met  
                   20                                  25                                  30

cac tgg tac cag cag aag tca ggc act tct ccc aaa ctc ttg att tat 144  
 His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Leu Leu Ile Tyr  
                   35                                  40                                  45

agc aca tcc aac ctg gct tct gga gtc cct tct cgc ttc agt ggc agt 192  
 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
                   50                                  55                                  60

ggg tct ggg acc ttt tat tct ctc aca atc agc agt gtg gag gct gaa 240  
 Gly Ser Gly Thr Phe Tyr Ser Leu Thr Ile Ser Ser Val Glu Ala Glu  
                   65                                  70                                  75                                  80

gat gct gcc gat tat tac tgc cat cag tgg agt agt tat cca tac acg 288  
 Asp Ala Ala Asp Tyr Tyr Cys His Gln Trp Ser Ser Tyr Pro Tyr Thr  
                                   85                                  90                                  95

ttc gga ggg ggg acc aag ctg gaa ata aaa 318  
 Phe Gly Gly Thr Lys Leu Glu Ile Lys  
                   100                                  105

<210> 25  
 <211> 106  
 <212> PRT  
 <213> Mus sp.

<400> 25

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Leu Gly  
 1                                  5                                  10                                  15

Glu Glu Ile Thr Leu Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met  
                   20                                  25                                  30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Leu Leu Ile Tyr  
                   35                                  40                                  45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
                   50                                  55                                  60

Gly Ser Gly Thr Phe Tyr Ser Leu Thr Ile Ser Ser Val Glu Ala Glu  
                   65                                  70                                  75                                  80

Asp Ala Ala Asp Tyr Tyr Cys His Gln Trp Ser Ser Tyr Pro Tyr Thr  
                                   85                                  90                                  95

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
                   100                                  105

<210> 26

<211> 360  
<212> DNA  
<213> Mus sp.

<220>  
<221> CDS  
<222> (1) .. (360)

<400> 26  
cag gtg cag ctg aag gag tct gga gct gag ctg atg aag cct ggg gcc 48  
Gln Val Gln Leu Lys Glu Ser Gly Ala Glu Leu Met Lys Pro Gly Ala  
1 5 10 15  
  
tca gtg aag ata tcc tgc aag gct act ggc tac aca ttc agt agc tac 96  
Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr  
20 25 30  
  
tgg ata gag tgg gta aag cag agg cct gga cat ggc ctt gag tgg att 144  
Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile  
35 40 45  
  
gga gag att tta cct gga agt ggt agt act aac tac aat gag aag ttc 192  
Gly Glu Ile Leu Pro Gly Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe  
50 55 60  
  
aag ggc aag gcc aca ttc act gca gat aca tcc tcc aac aca gcc tac 240  
Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr  
65 70 75 80  
  
atg caa ctc agc agc ctg aca tct gag gac tct gcc gtc tat tac tgt 288  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95  
  
gca aga gac agg aac ggc tac gtg aac tac ttt gac tcc tgg ggc caa 336  
Ala Arg Asp Arg Asn Gly Tyr Val Asn Tyr Phe Asp Ser Trp Gly Gln  
100 105 110  
  
ggc acc act ctc aca gtc tcc tca 360  
Gly Thr Thr Leu Thr Val Ser Ser  
115 120

<210> 27  
<211> 120  
<212> PRT  
<213> Mus sp.

<400> 27  
Gln Val Gln Leu Lys Glu Ser Gly Ala Glu Leu Met Lys Pro Gly Ala  
1 5 10 15  
  
Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Ser Tyr  
20 25 30  
  
Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile  
35 40 45

Gly Glu Ile Leu Pro Gly Ser Gly Ser Thr Asn Tyr Asn Glu Lys Phe  
50 55 60

Lys Gly Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr  
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asp Arg Asn Gly Tyr Val Asn Tyr Phe Asp Ser Trp Gly Gln  
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser  
115 120

<210> 28  
<211> 351  
<212> DNA  
<213> Mus sp.

<220>  
<221> CDS  
<222> (1) .. (351)

<400> 28  
gat gtg aag ctt cag gag tca gga cct gac ctg gtg aaa cct tct cag 48  
Asp Val Lys Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln  
1 5 10 15  
  
tca ctt tca ctc acc tgc act gtc act ggc tac tcc atc acc agt ggt 96  
Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly  
20 25 30  
  
tat agc tgg cac tgg atc cgg cag ttt cca gga aac aaa ctg gaa tgg 144  
Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp  
35 40 45  
  
atg ggc tac ata cac tac agt ggt agc act aag tac aac cca tct ctc 192  
Met Gly Tyr Ile His Tyr Ser Gly Ser Thr Lys Tyr Asn Pro Ser Leu  
50 55 60  
  
aaa agt cga atc tct atc act cga gac aca tcc aag aac cag ttc ttc 240  
Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe  
65 70 75 80  
  
ctg cag ttg aat tct gtg act act gag gac aca gcc aca tat tac tgt 288  
Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys  
85 90 95  
  
gca aga ctc tgg agt tgg tac ttc gat gtc tgg ggc gca ggg acc acg 336  
Ala Arg Leu Trp Ser Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr  
100 105 110  
  
gtc acc gtc tcc tca 351

Val Thr Val Ser Ser  
115

<210> 29  
<211> 117  
<212> PRT  
<213> Mus sp.

<400> 29

Asp Val Lys Leu Gln Glu Ser Gly Pro Asp Leu Val Lys Pro Ser Gln  
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly  
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp  
35 40 45

Met Gly Tyr Ile His Tyr Ser Gly Ser Thr Lys Tyr Asn Pro Ser Leu  
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe  
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys  
85 90 95

Ala Arg Leu Trp Ser Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Thr  
100 105 110

Val Thr Val Ser Ser  
115

<210> 30  
<211> 336  
<212> DNA  
<213> Mus sp.

<220>  
<221> CDS  
<222> (1)..(336)

<400> 30

aac att atg atg aca cag tcg cca tca tct ctg gct gtg tct gca gga 48  
Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly  
1 5 10 15

gaa aag gtc act atg agc tgt aag tcc agt caa agt gtt tta tac agt 96  
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

tca aat cag aag aac tac ttg gcc tgg tac cag cag aaa cca ggg cag 144  
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggt gtc 192  
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

cct gat cgc ttc aca ggc agt gga tct ggg aca gat ttt act ctt acc 240  
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

atc agc agt gta caa gct gaa gac ctg gca gtt tat tac tgt cat caa 288  
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His Gln  
85 90 95

tac ctc tcc tcg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 336  
Tyr Leu Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105 110

<210> 31  
<211> 112  
<212> PRT  
<213> Mus sp.

<400> 31

Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly  
1 5 10 15

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
20 25 30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln  
35 40 45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys His Gln  
85 90 95

Tyr Leu Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105 110

<210> 32  
<211> 57  
<212> DNA  
<213> Unknown

<220>  
<223> Signal sequence peptide

<220>  
<221> CDS  
<222> (1)..(57)

<400> 32  
atg gct tgg gtg tgg acc ttg cta ttc ctg atg gca gct gcc caa agt 48  
Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser  
1 5 10 15  
  
gcc caa gca 57  
Ala Gln Ala

<210> 33  
<211> 19  
<212> PRT  
<213> Unknown

<220>  
<223> Synthetic Construct

<400> 33  
Met Ala Trp Val Trp Thr Leu Leu Phe Leu Met Ala Ala Ala Gln Ser  
1 5 10 15

Ala Gln Ala

<210> 34  
<211> 60  
<212> DNA  
<213> Unknown

<220>  
<223> Signal sequence peptide

<220>  
<221> CDS  
<222> (1)..(60)

<400> 34  
atg gaa tca cag act cag gtc ttc ctc tcc ctg ctg ctc tgg ata tct 48  
Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Ile Ser  
1 5 10 15  
  
ggc acc tgt ggc 60  
Gly Thr Cys Gly  
20

<210> 35  
<211> 20

<212> PRT  
<213> Unknown

<220>  
<223> Synthetic Construct

<400> 35

Met	Glu	Ser	Gln	Thr	Gln	Val	Phe	Leu	Ser	Leu	Leu	Leu	Trp	Ile	Ser
1				5					10					15	

Gly	Thr	Cys	Gly
			20